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RAW SEQUENCE LISTING

DATE: 09/25/2000

PATENT APPLICATION: US/09/662,293

TIME: 15:45:21

Input Set : A:\A1-2-c41.app

Output Set: N:\CRF3\09252000\I662293.raw

3 <110> APPLICANT: McCall, Catherine A.
4 Hunter, Shirley Wu
5 Weber, Eric R.
7 <120> TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
8 AND USES THEREOF
10 <130> FILE REFERENCE: AL-2-C4
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/662,293
13 <141> CURRENT FILING DATE: 2000-09-14
15 <150> PRIOR APPLICATION NUMBER: 09/292,225
16 <151> PRIOR FILING DATE: 1999-04-15
18 <150> PRIOR APPLICATION NUMBER: 60/098,909
19 <151> PRIOR FILING DATE: 1998-09-02
21 <150> PRIOR APPLICATION NUMBER: 60/085,295
22 <151> PRIOR FILING DATE: 1998-05-13
24 <150> PRIOR APPLICATION NUMBER: 60/098,565
25 <151> PRIOR FILING DATE: 1998-04-17
27 <150> PRIOR APPLICATION NUMBER: 09/062,013
28 <151> PRIOR FILING DATE: 1998-04-17
30 <160> NUMBER OF SEQ ID NOS: 57
32 <170> SOFTWARE: PatentIn Ver. 2.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 14
36 <212> TYPE: PRT
37 <213> ORGANISM: Dermatophagoides farinae
39 <400> SEQUENCE: 1
40 Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro Met
41 1 5 10
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 20
46 <212> TYPE: PRT
47 <213> ORGANISM: Dermatophagoides farinae
49 <400> SEQUENCE: 2
50 Asp Tyr Glu Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ala Pro Leu
51 1 5 10 15
53 Tyr Lys Arg Pro
54 20
57 <210> SEQ ID NO: 3
58 <211> LENGTH: 20
59 <212> TYPE: PRT
60 <213> ORGANISM: Dermatophagoides farinae
62 <400> SEQUENCE: 3
63 Asp Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Ser
64 1 5 10 15
66 Val Asn Gly Gly
67 20
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 20

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72 <212> TYPE: PRT
73 <213> ORGANISM: Dermatophagoides farinae
75 <400> SEQUENCE: 4
76 Asp Pro Ala Lys Gly Met Ser Pro Pro Gly Phe Ile Val Gly Glu Glu
77   1           5           10           15
79 Gly Val Leu Ser
80           20
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 12
85 <212> TYPE: PRT
86 <213> ORGANISM: Dermatophagoides farinae
88 <400> SEQUENCE: 5
89 Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro
90   1           5           10
93 <210> SEQ ID NO: 6
94 <211> LENGTH: 18
95 <212> TYPE: PRT
96 <213> ORGANISM: Dermatophagoides farinae
98 <400> SEQUENCE: 6
99 Asp Ala Phe Glu Pro His Gly Tyr Leu Leu Thr Ala Ala Val Ser Pro
100  1           5           10           15
102 Gly Lys
106 <210> SEQ ID NO: 7
107 <211> LENGTH: 13
108 <212> TYPE: PRT
109 <213> ORGANISM: Dermatophagoides farinae
111 <400> SEQUENCE: 7
112 Asp Lys Gln Asn Tyr Leu Ala Leu Val Arg Glu Leu Lys
113  1           5           10
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 24
118 <212> TYPE: PRT
119 <213> ORGANISM: Dermatophagoides farinae
121 <400> SEQUENCE: 8
122 Asp Met Ala Gln Asn Tyr Lys Tyr Arg Gln Gln Phe Ile Gln Ser Val
123  1           5           10           15
125 Leu Asn Asn Gly Ala Thr Arg Gln
126           20
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 23
131 <212> TYPE: PRT
132 <213> ORGANISM: Dermatophagoides farinae
134 <220> FEATURE:
135 <223> OTHER INFORMATION: At locations 3 and 7, Xaa = any amino acid
137 <400> SEQUENCE: 9
W--> 138 Asp Glu Xaa Asn Val Met Xaa Tyr Val Leu Tyr Thr Met His Tyr Tyr
139   1           5           10           15
141 Leu Asn Asn Gly Ala Thr Arg
142           20

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145 <210> SEQ ID NO: 10
146 <211> LENGTH: 17
147 <212> TYPE: PRT
148 <213> ORGANISM: Dermatophagoides farinae
150 <220> FEATURE:
151 <223> OTHER INFORMATION: At location 14, Xaa = any amino acid
153 <400> SEQUENCE: 10
W--> 154 Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Xaa Ser Ile
      155      1          5          10          15
      157 Glu
161 <210> SEQ ID NO: 11
162 <211> LENGTH: 19
163 <212> TYPE: PRT
164 <213> ORGANISM: Dermatophagoides farinae
166 <400> SEQUENCE: 11
167 Asp Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Ser
168      1          5          10          15
170 Val Asn Gly
174 <210> SEQ ID NO: 12
175 <211> LENGTH: 18
176 <212> TYPE: PRT
177 <213> ORGANISM: Dermatophagoides farinae
179 <400> SEQUENCE: 12
180 Asp Tyr Ala Lys Asn Pro Lys Arg Ile Val Cys Ile Val Gly Thr Glu
181      1          5          10          15
183 Gly Val
187 <210> SEQ ID NO: 13
188 <211> LENGTH: 20
189 <212> TYPE: PRT
190 <213> ORGANISM: Dermatophagoides farinae
192 <400> SEQUENCE: 13
193 Asp Pro Ala Lys Gly Met Ser Pro Pro Gly Phe Ile Val Gly Glu Glu
194      1          5          10          15
196 Gly Val Leu Ser
197      20
200 <210> SEQ ID NO: 14
201 <211> LENGTH: 1752
202 <212> TYPE: DNA
203 <213> ORGANISM: Dermatophagoides farinae
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (1)..(1665)
209 <400> SEQUENCE: 14
210 atg aaa acc ata tat gca ata ctt agt att atg gcc tgc att ggc ctt 48
211 Met Lys Thr Ile Tyr Ala Ile Leu Ser Ile Met Ala Cys Ile Gly Leu
212      1          5          10          15
214 atg aat gca tcc atc aaa cga gat cat aat gat tat tcg aaa aat ccg 96
215 Met Asn Ala Ser Ile Lys Arg Asp His Asn Asp Tyr Ser Lys Asn Pro
216      20          25          30

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218 atg aga att gtt tgt tat gtt gga aca tgg tcc gta tat cat aaa gtt 144
219 Met Arg Ile Val Cys Tyr Val Gly Thr Trp Ser Val Tyr His Lys Val
220          35          40          45
222 gat cca tac act atc gaa gat att gat cca ttc aag tgt aca cat tta 192
223 Asp Pro Tyr Thr Ile Glu Asp Ile Asp Pro Phe Lys Cys Thr His Leu
224          50          55          60
226 atg tat ggt ttc gct aaa att gat gaa tac aaa tac aca att caa gtt 240
227 Met Tyr Gly Phe Ala Lys Ile Asp Glu Tyr Lys Tyr Thr Ile Gln Val
228          65          70          75          80
230 ttc gat cct tac caa gat gat aac cat aac tca tgg gaa aaa cgt ggt 288
231 Phe Asp Pro Tyr Gln Asp Asp Asn His Asn Ser Trp Glu Lys Arg Gly
232          85          90          95
234 tat gaa cgt ttc aac aac ttg cga ttg aag aat cca gaa tta acc acc 336
235 Tyr Glu Arg Phe Asn Asn Leu Arg Leu Lys Asn Pro Glu Leu Thr Thr
236          100          105          110
238 atg att tca ctt ggt ggt tgg tat gaa ggc tcg gaa aaa tat tcc gat 384
239 Met Ile Ser Leu Gly Gly Trp Tyr Glu Gly Ser Glu Lys Tyr Ser Asp
240          115          120          125
242 atg gct gca aat cca aca tat cgt caa caa ttc ata caa tca gtt ttg 432
243 Met Ala Ala Asn Pro Thr Tyr Arg Gln Gln Phe Ile Gln Ser Val Leu
244          130          135          140
246 gac ttt ttg caa gaa tac aag ttc gac ggt cta gat ttg gat tgg gag 480
247 Asp Phe Leu Gln Glu Tyr Lys Phe Asp Gly Leu Asp Leu Asp Trp Glu
248          145          150          155          160
250 tat cct gga tct cga ttg ggt aac ccg aaa atc gat aaa caa aac tat 528
251 Tyr Pro Gly Ser Arg Leu Gly Asn Pro Lys Ile Asp Lys Gln Asn Tyr
252          165          170          175
254 ttg gct ttg gtt aga gaa ctt aaa gac gct ttt gaa cct cat ggc tac 576
255 Leu Ala Leu Val Arg Glu Leu Lys Asp Ala Phe Glu Pro His Gly Tyr
256          180          185          190
258 ttg ttg act gct gca gta tca cca ggt aaa gac aaa atc gac cga gct 624
259 Leu Leu Thr Ala Ala Val Ser Pro Gly Lys Asp Lys Ile Asp Arg Ala
260          195          200          205
262 tat gat atc aaa gaa ttg aac aaa ttg ttc gat tgg atg aat gtc atg 672
263 Tyr Asp Ile Lys Glu Leu Asn Lys Leu Phe Asp Trp Met Asn Val Met
264          210          215          220
266 aca tat gat tac cac ggt gga tgg gaa aac ttt tac ggt cac aat gct 720
267 Thr Tyr Asp Tyr His Gly Gly Trp Glu Asn Phe Tyr Gly His Asn Ala
268          225          230          235          240
270 ccg ttg tat aaa cga cca gat gaa act gat gag ttg cac act tac ttc 768
271 Pro Leu Tyr Lys Arg Pro Asp Glu Thr Asp Glu Leu His Thr Tyr Phe
272          245          250          255
274 aat gtc aac tac acc atg cac tat tat ttg aac aat ggt gcc acc aga 816
275 Asn Val Asn Tyr Thr Met His Tyr Tyr Leu Asn Asn Gly Ala Thr Arg
276          260          265          270
278 gac aaa ttg gta atg ggt gtt cca ttc tat ggc cgt gct tgg agc att 864
279 Asp Lys Leu Val Met Gly Val Pro Phe Tyr Gly Arg Ala Trp Ser Ile
280          275          280          285
282 gaa gat cga agc aaa ctc aaa ctt gga gat cca gcc aaa ggc atg tcg 912

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```

283 Glu Asp Arg Ser Lys Leu Lys Leu Gly Asp Pro Ala Lys Gly Met Ser
284      290      295      300
286 ccc cca ggt ttc att tct ggt gaa gaa ggt gtc ctc tca tat ata gaa 960
287 Pro Pro Gly Phe Ile Ser Gly Glu Glu Gly Val Leu Ser Tyr Ile Glu
288 305      310      315      320
290 ttg tgt caa ttg ttt caa aaa gaa gaa tgg cat atc caa tac gat gaa 1008
291 Leu Cys Gln Leu Phe Gln Lys Glu Glu Trp His Ile Gln Tyr Asp Glu
292      325      330      335
294 tat tac aat gct cca tat ggt tac aat gat aaa atc tgg gtc ggt tac 1056
295 Tyr Tyr Asn Ala Pro Tyr Gly Tyr Asn Asp Lys Ile Trp Val Gly Tyr
296      340      345      350
298 gat gat ctg gcc agt ata tca tgc aag ttg gct ttc ctg aaa gaa tta 1104
299 Asp Asp Leu Ala Ser Ile Ser Cys Lys Leu Ala Phe Leu Lys Glu Leu
300      355      360      365
302 ggc gtt tct ggt gtc atg gtt tgg tca ttg gaa aat gat gat ttc aaa 1152
303 Gly Val Ser Gly Val Met Val Trp Ser Leu Glu Asn Asp Asp Phe Lys
304      370      375      380
306 ggt cac tgc gga ccg aaa aat cca ttg ttg aac aaa gtt cat aat atg 1200
307 Gly His Cys Gly Pro Lys Asn Pro Leu Leu Asn Lys Val His Asn Met
308 385      390      395      400
310 att aat ggc gat gaa aag aac tct ttc gaa tgc att ttg ggt cca agt 1248
311 Ile Asn Gly Asp Glu Lys Asn Ser Phe Glu Cys Ile Leu Gly Pro Ser
312      405      410      415
314 aca acg aca cca act cca acg acg aca ccc aca acc ccg act aca acg 1296
315 Thr Thr Thr Pro Thr Pro Thr Thr Pro Thr Thr Pro Thr Thr Thr
316      420      425      430
318 cca aca act cct tct ccc acc acc ccg aca aca acc cct tct ccc acc 1344
319 Pro Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Pro Ser Pro Thr
320      435      440      445
322 acc ccg aca aca acc cct tct ccc acc aca ccg aca aca act cct tct 1392
323 Thr Pro Thr Thr Thr Pro Ser Pro Thr Thr Pro Thr Thr Pro Ser
324      450      455      460
326 ccc acc aca cca aca cca aca aca cca aca cca gcc cct aca aca tcg 1440
327 Pro Thr Thr Pro Thr Pro Thr Thr Pro Thr Pro Ala Pro Thr Thr Ser
328 465      470      475      480
330 aca cct tcg cca acc acg acc gaa cac aca agc gaa aca cca aaa tat 1488
331 Thr Pro Ser Pro Thr Thr Thr Glu His Thr Ser Glu Thr Pro Lys Tyr
332      485      490      495
334 aca acc tat gtc gat gga cat ctt atc aaa tgt tac aag gaa ggt gat 1536
335 Thr Thr Tyr Val Asp Gly His Leu Ile Lys Cys Tyr Lys Glu Gly Asp
336      500      505      510
338 atc cca cat cca acc aat ata cac aaa tat ttg gtc tgt gaa ttt gtt 1584
339 Ile Pro His Pro Thr Asn Ile His Lys Tyr Leu Val Cys Glu Phe Val
340      515      520      525
342 aat ggt ggc tgg tgg gtt cat att atg ccc tgt cca ccg ggc act att 1632
343 Asn Gly Gly Trp Trp Val His Ile Met Pro Cys Pro Pro Gly Thr Ile
344      530      535      540
346 tgg tgt caa gaa aaa ttg act tgt ata ggc gaa taattctgaa aaaaaaatc 1685
347 Trp Cys Gln Glu Lys Leu Thr Cys Ile Gly Glu

```

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY

DATE: 09/25/2000

PATENT APPLICATION: US/09/662,293

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Input Set : A:\A1-2-c41.app

Output Set: N:\CRF3\09252000\I662293.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:138 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:154 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:154 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:154 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:1107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:1127 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1127 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1127 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1147 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1147 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1147 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1176 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:1176 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1176 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1192 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1192 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:1192 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:1247 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1247 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:1247 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:1247 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:1247 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
L:2210 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2210 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2210 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46

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